

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 19, 2003, 09:07:27 ; Search time 5123 Seconds
(without alignments)
16410.167 Million cell updates/sec

Title: US-09-804-060-1
Perfect score: 2055
Sequence: 1 tttctgtgtttctcgaaact.....cccgacggcgatggcattga 2055

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*

DNA Search
Using SEQ 1

seq 3 is a fragment
→ would have found in
attached oligo search.

28: em_un:*
 29: em_vi:*
 30: em_htg_hum:*
 31: em_htg_inv:*
 32: em_htg_other:*
 33: em_htg_mus:*
 34: em_htg_pln:*
 35: em_htg_rod:*
 36: em_htg_mam:*
 37: em_htg_vrt:*
 38: em_sy:*
 39: em_htgo_hum:*
 40: em_htgo_mus:*
 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
	1	2055	100.0	2055	6	AX394566	Sequence
	2	2055	100.0	340000	1	AP005274	Corynebac
	3	2055	100.0	349980	6	AX120085	Sequence
	4	1653	80.4	1653	6	AX120161	Sequence
	5	1653	80.4	1653	6	BD162278	Novel pol
c	6	717.6	34.9	87340	1	AP005224	Corynebac
c	7	570	27.7	570	6	AX120162	Sequence
c	8	570	27.7	570	6	BD162279	Novel pol
	9	481	23.4	481	6	AX394568	Sequence
	10	400	19.5	1056	6	AX394318	Sequence
	11	200	9.7	654	6	AX120163	Sequence
	12	200	9.7	654	6	BD162280	Novel pol
c	13	132.6	6.5	295150	1	SCO939125	Streptomy
	14	129.2	6.3	300550	1	AP005030	Streptomy
c	15	92	4.5	601	6	AX066027	Sequence
	16	70.6	3.4	281450	1	AP005032	Streptomy
c	17	64.4	3.1	125020	9	AF429315	Homo sapi
c	18	62.6	3.0	300100	1	SCO939123	Streptomy
c	19	56.6	2.8	298450	1	SCO939107	Streptomy
c	20	55.6	2.7	3051	1	ARU9587	Prauserel
c	21	52	2.5	2000	6	AX655393	Sequence
	22	51	2.5	318	6	AX394320	Sequence
	23	49.4	2.4	125020	9	AF429315	Homo sapi
	24	49	2.4	2000	6	AX655393	Sequence
	25	45.8	2.2	683	6	AX435926	Sequence
	26	45.4	2.2	10114	1	AE014368	Brucella
	27	44.4	2.2	301056	1	AE016999	Bacillus
c	28	44.2	2.2	12695	1	AE004164	Vibrio ch
c	29	43.8	2.1	13507	1	AE009571	Brucella
c	30	43.2	2.1	303650	1	AP001519	Bacillus
	31	42.8	2.1	10264	1	AE000167	Escherich
	32	42.8	2.1	12242	1	AE005241	Escherich
	33	42.8	2.1	16962	1	D90702	Escherichia

Nockel

Nakagawa

wo 02/18427
 GenBank
 EP 1108790

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OM nucleic - nucleic search, using sw model

Run on: December 19, 2003, 09:07:27 ; Search time 415 Seconds
(without alignments)
13367.097 Million cell updates/sec

Title: US-09-804-060-1
Perfect score: 2055
Sequence: 1 tttctgtgtttctcgaaact.....cccgacggcgatggcattga 2055

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_19Jun03:*

- 1: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
- 2: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
- 3: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
- 4: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
- 5: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
- 6: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
- 7: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
- 8: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*
- 9: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*
- 10: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:*
- 11: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*
- 12: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
- 13: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*
- 14: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*
- 15: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*
- 16: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*
- 17: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:*
- 18: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:*
- 19: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*
- 20: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
- 21: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
- 22: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
- 23: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
- 24: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
- 25: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match Length	DB	ID	Mockel ↑	Description
	1	2055	100.0	2055	24	AAD35061	Corynebacterium gl
	2	2055	100.0	349980	22	AAH64966	C glutamicum codin
	3	1653	80.4	1653	22	AAH65042	C glutamicum codin
	4	1653	80.4	1653	25	ACA01845	C. glutamicum deri
c	5	570	27.7	570	22	AAH65043	C glutamicum codin
	6	481	23.4	481	24	AAD35062	Corynebacterium gl
	7	400	19.5	1056	24	AAD27952	Corynebacterium gl
	8	200	9.7	654	22	AAH65044	C glutamicum codin
	9	200	9.7	654	25	ACA01846	C. glutamicum deri
c	10	92	4.5	601	22	AAF71323	Corynebacterium gl
	11	51	2.5	318	24	AAD27953	Corynebacterium gl
	12	45.8	2.2	683	24	ABK77050	Bacillus lichenifo
c	13	42.4	2.1	3016	24	ABT05460	DNA of NOVX 8a SEQ
c	14	42	2.0	2895	22	AAI67200	Nucleotide sequenc
c	15	42	2.0	2897	22	AAH78221	Nucleotide sequenc
	16	41.4	2.0	651	24	ABK89545	DNA encoding M. tu
c	17	41.4	2.0	4403765	22	AAI99683	Mycobacterium tube
c	18	41.4	2.0	4411529	22	AAI99682	Mycobacterium tube
	19	41.2	2.0	17091	20	AAX60096	Acetobacter xylinu
c	20	41	2.0	632	25	ABT16477	Human intracellula
c	21	40.8	2.0	1210	25	ABZ59737	Human secreted pro
c	22	40.8	2.0	2992	24	ABT05461	DNA of NOVX 8b SEQ
c	23	40.8	2.0	3137	24	ABS52094	Human EGF-Related
c	24	40.8	2.0	3877	25	ABZ22653	Human epidermal gr
	25	40.6	2.0	1302	24	ABQ69441	Listeria innocua D
	26	40.6	2.0	1362	24	ABQ67807	Listeria innocua D
	27	40.6	2.0	1163020	24	ABQ67197	Listeria innocua c
	28	40.6	2.0	3011208	24	ABQ69245	Listeria innocua D
	29	39.2	1.9	546	19	AAT76906	S. glaucescens acb
	30	39.2	1.9	6854	19	AAT76903	S. glaucescens Pst
	31	37.2	1.8	75216	24	ABX09141	Mycobacterium tube
	32	37.2	1.8	90600	24	ABQ78872	S. roseosporus dap
	33	37.2	1.8	4403765	22	AAI99683	Mycobacterium tube
	34	37.2	1.8	4411529	22	AAI99682	Mycobacterium tube
	35	37	1.8	3849	22	AAF25795	S. chrysomallus ac
	36	37	1.8	198285	24	ABK84699	Human cDNA differe
	37	37	1.8	198285	24	ABN97319	Gene #3817 used to
	38	36.8	1.8	1698	23	ABL05453	Drosophila melanog
c	39	36.8	1.8	3698	23	ABL05452	Drosophila melanog
	40	36.4	1.8	558	24	ABL01541	Murine apoptosis r
c	41	36.2	1.8	991	23	AAS82060	DNA encoding novel
c	42	36.2	1.8	991	23	AAS90317	DNA encoding novel
	43	36.2	1.8	1632	22	AAH81447	Escherichia coli p
	44	36.2	1.8	2262	20	AAX23322	N. meningitidis st
	45	36	1.8	1815	23	AAS78487	DNA encoding novel

ALIGNMENTS

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OM nucleic - nucleic search, using sw model

Run on: December 19, 2003, 09:07:27 ; Search time 2983 Seconds
(without alignments)
16743.446 Million cell updates/sec.

Title: US-09-804-060-1
Perfect score: 2055
Sequence: 1 tttctgtgtttctcgaaact.....cccgacggcgatggcattga 2055

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

- 1: em_estba:*
- 2: em_esthum:*
- 3: em_estin:*
- 4: em_estmu:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_htc:*
- 9: gb_est1:*
- 10: gb_est2:*
- 11: gb_htc:*
- 12: gb_est3:*
- 13: gb_est4:*
- 14: gb_est5:*
- 15: em_estfun:*
- 16: em_estom:*
- 17: em_gss_hum:*
- 18: em_gss_inv:*
- 19: em_gss_pln:*
- 20: em_gss_vrt:*
- 21: em_gss_fun:*
- 22: em_gss_mam:*
- 23: em_gss_mus:*
- 24: em_gss_pro:*
- 25: em_gss_rod:*
- 26: em_gss_phg:*
- 27: em_gss_vrl:*

28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	%		DB	ID	Description
			Query	Match Length			
c	1	55	2.7	1201	13	BX381961	BX381961 BX381961
c	2	45.4	2.2	456	10	BE490732	BE490732 WHE0369_B
c	3	45.4	2.2	563	6	AL815463	AL815463 Triticum
c	4	45	2.2	839	29	CNS004NB	AL054280 Drosophil
c	5	42.8	2.1	615	12	BJ063236	BJ063236 BJ063236
	6	42	2.0	885	13	BX425603	BX425603 BX425603
	7	41	2.0	1201	13	BX359002	BX359002 BX359002
	8	40.8	2.0	449	28	BH224792	BH224792 1006121E0
	9	40.8	2.0	466	28	BH234414	BH234414 1006179B0
	10	40.8	2.0	484	28	BH221656	BH221656 1006102E0
	11	40.8	2.0	491	28	BH221697	BH221697 1006102G0
	12	40.8	2.0	525	28	BH234159	BH234159 1006177G0
	13	40.8	2.0	525	28	BH234162	BH234162 1006177G1
	14	40.8	2.0	525	28	BH407208	BH407208 1007006B0
	15	40.8	2.0	546	28	BH221583	BH221583 1006102B0
	16	40.8	2.0	550	29	CC037351	CC037351 3591_1_87
	17	40.8	2.0	556	28	BH221712	BH221712 1006102H0
	18	40.8	2.0	597	28	BH234040	BH234040 1006177B1
	19	40.8	2.0	604	28	BH220570	BH220570 1006095D1
	20	40.8	2.0	609	29	CC024006	CC024006 3591_1_37
	21	40.8	2.0	628	28	BH215894	BH215894 1006038C0
	22	40.8	2.0	635	28	BH234021	BH234021 1006177A1
	23	40.8	2.0	647	29	CC024803	CC024803 3591_1_40
	24	40.8	2.0	1101	29	CNS000D1	AL065414 Drosophil
c	25	40.8	2.0	1122	13	BQ721681	BQ721681 AGENCOURT
	26	40.4	2.0	747	29	BZ502041	BZ502041 BONQB29TR
	27	40.2	2.0	658	10	BG320883	BG320883 Zm04_09a1
c	28	40	1.9	601	14	CB411877	CB411877 TgESTzyh5
c	29	39.6	1.9	448	28	BH872480	BH872480 hp05h09.g
c	30	39.6	1.9	727	10	BG724455	BG724455 EST0012 D
	31	39.6	1.9	1201	9	AL574305	AL574305 AL574305
	32	39.2	1.9	505	28	BH221669	BH221669 1006102F0
	33	39.2	1.9	519	29	CC024522	CC024522 3591_1_39
c	34	39.2	1.9	1201	13	BX460099	BX460099 BX460099
c	35	39	1.9	457	13	BQ761662	BQ761662 EBem10 SQ
	36	38.8	1.9	1201	13	BX381961	BX381961 BX381961
c	37	38.6	1.9	354	10	BG279060	BG279060 a9ellnp.r
	38	38.6	1.9	496	12	BM380593	BM380593 MEST522-B
	39	38.6	1.9	639	10	BE040761	BE040761 OF11C01 O
	40	38.6	1.9	710	29	BZ616299	BZ616299 ig58d07.g
c	41	38.6	1.9	755	14	CD440002	CD440002 EL01N0531
c	42	38.6	1.9	832	12	BJ291473	BJ291473 BJ291473
	43	38.6	1.9	847	13	BU613082	BU613082 UI-M-FR0-
	44	38.6	1.9	2362	11	AK080615	AK080615 Mus muscu
c	45	38.4	1.9	541	10	BE150908	BE150908 RC4-HT027

OM nucleic - nucleic search, using sw model

Run on: December 19, 2003, 09:07:27 ; Search time 211 Seconds
(without alignments)
4298.779 Million cell updates/sec

Title: US-09-804-060-1
Perfect score: 2055
Sequence: 1 tttctgtgtttctcgaaact.....cccgacggcgatggcattga 2055

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%				ID	Description
	No.	Score	Match	Length	DB	Query		
c	1	41.4	2.0	4403765	3	US-09-103-840A-2		Sequence 2, Appli
c	2	41.4	2.0	4411529	3	US-09-103-840A-1		Sequence 1, Appli
	3	39.2	1.9	546	4	US-09-194-905-3		Sequence 3, Appli
	4	39.2	1.9	6854	4	US-09-194-905-7		Sequence 7, Appli
c	5	37.6	1.8	7218	1	US-08-232-463-14		Sequence 14, Appl
	6	37.2	1.8	1596	4	US-09-252-991A-10119		Sequence 10119, A
	7	37.2	1.8	2400	4	US-09-252-991A-10051		Sequence 10051, A
	8	37.2	1.8	4403765	3	US-09-103-840A-2		Sequence 2, Appli
	9	37.2	1.8	4411529	3	US-09-103-840A-1		Sequence 1, Appli
c	10	35.6	1.7	423	4	US-09-252-991A-606		Sequence 606, App
c	11	35.6	1.7	1038	4	US-09-252-991A-560		Sequence 560, App

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OM nucleic - nucleic search, using sw model

Run on: December 19, 2003, 10:37:23 ; Search time 1183 Seconds
(without alignments)
5788.401 Million cell updates/sec

Title: US-09-804-060-1
Perfect score: 2055
Sequence: 1 tttctgtgtttctcgaaact.....cccgacggcgatggcattga 2055

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2211978 seqs, 1666101734 residues

Total number of hits satisfying chosen parameters: 4423956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq2:*
14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Appl. ↑

Nakagawa
 USPAP 20020197605
 SEQ ID NO: 1 is entire seq
 73x10⁶ bp
 = EP1101790

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2055	100.0	2055	9	US-09-804-060-1	Sequence 1, Appli
2	2055	100.0	3309400	10	US-09-738-626-1	Sequence 1, Appli
3	1653	80.4	1653	10	US-09-738-626-77	Sequence 77, Appl
c 4	570	27.7	570	10	US-09-738-626-78	Sequence 78, Appl
5	481	23.4	481	9	US-09-804-060-3	Sequence 3, Appli
6	200	9.7	654	10	US-09-738-626-79	Sequence 79, Appl
7	129.2	6.3	1725	15	US-10-156-761-2417	Sequence 2417, Ap
8	129.2	6.3	9025608	15	US-10-156-761-1	Sequence 1, Appli
9	70.6	3.4	1695	15	US-10-156-761-2803	Sequence 2803, Ap
10	45.8	2.2	683	10	US-09-974-300-4341	Sequence 4341, Ap
11	45	2.2	690	15	US-10-156-761-2422	Sequence 2422, Ap
12	44.2	2.2	1049	13	US-10-140-472-358	Sequence 358, App
13	44.2	2.2	1049	13	US-10-141-761-358	Sequence 358, App
14	44.2	2.2	1049	13	US-10-142-885-358	Sequence 358, App
15	44.2	2.2	1049	13	US-10-158-790-358	Sequence 358, App
16	44.2	2.2	1049	13	US-10-137-871-358	Sequence 358, App
17	44.2	2.2	1049	13	US-10-140-805-358	Sequence 358, App
18	44.2	2.2	1049	13	US-10-140-864-358	Sequence 358, App
19	44.2	2.2	1049	13	US-10-140-923-358	Sequence 358, App
20	44.2	2.2	1049	13	US-10-141-756-358	Sequence 358, App
21	44.2	2.2	1049	13	US-10-141-759-358	Sequence 358, App
22	44.2	2.2	1049	15	US-10-123-155-358	Sequence 358, App
23	44.2	2.2	1049	16	US-10-146-731-358	Sequence 358, App
24	43.4	2.1	675	15	US-10-156-761-2804	Sequence 2804, Ap
c 25	42	2.0	2895	13	US-10-239-663-25	Sequence 25, Appl
c 26	42	2.0	2897	13	US-10-221-097-25	Sequence 25, Appl
c 27	40.8	2.0	1210	11	US-09-901-152-1	Sequence 1, Appli
c 28	40.8	2.0	2992	13	US-10-406-073-1	Sequence 1, Appli
c 29	40.8	2.0	3791	15	US-10-195-142-1	Sequence 1, Appli
c 30	40.8	2.0	3877	13	US-09-855-824-1	Sequence 1, Appli
c 31	40.4	2.0	750	15	US-10-195-142-7	Sequence 7, Appli
c 32	40.4	2.0	2967	15	US-10-195-142-3	Sequence 3, Appli
33	39.2	1.9	520	15	US-10-184-644-332	Sequence 332, App
34	39.2	1.9	520	15	US-10-184-634-332	Sequence 332, App
35	39.2	1.9	546	10	US-09-922-683-3	Sequence 3, Appli
36	39.2	1.9	6854	10	US-09-922-683-7	Sequence 7, Appli
37	38.8	1.9	1287	15	US-10-156-761-2905	Sequence 2905, Ap
c 38	38.8	1.9	9025608	15	US-10-156-761-1	Sequence 1, Appli
39	37.2	1.8	75216	16	US-10-080-170-646	Sequence 646, App
40	37	1.8	444	13	US-10-140-472-498	Sequence 498, App
41	37	1.8	444	13	US-10-141-761-498	Sequence 498, App
42	37	1.8	444	13	US-10-142-885-498	Sequence 498, App
43	37	1.8	444	13	US-10-158-790-498	Sequence 498, App
44	37	1.8	444	13	US-10-137-871-498	Sequence 498, App
45	37	1.8	444	13	US-10-140-805-498	Sequence 498, App

ALIGNMENTS

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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 19, 2003, 09:05:58 ; Search time 5915 Seconds
(without alignments)
3810.854 Million cell updates/sec

Title: US-09-804-060-2
Perfect score: 2773
Sequence: 1 MSVGGSDWKNFKEVDIIRFA.....IDRGTEDGAVFGVKLPGVME 551

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

*DNA Regular Search
using SEQ 2
(translated)*

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh

Q=/cgn2_1/USPTO_spool/US09804060/runat_19122003_090552_8503/app_query.fasta_1.71
1

-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09804060_@CGN_1_1_3635_@runat_19122003_090552_8503 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*

11: gb_sts:*
 12: gb_sy:*
 13: gb_un:*
 14: gb_vi:*
 15: em_ba:*
 16: em_fun:*
 17: em_hum:*
 18: em_in:*
 19: em_mu:*
 20: em_om:*
 21: em_or:*
 22: em_ov:*
 23: em_pat:*
 24: em_ph:*
 25: em_pl:*
 26: em_ro:*
 27: em_sts:*
 28: em_un:*
 29: em_vi:*
 30: em_htg_hum:*
 31: em_htg_inv:*
 32: em_htg_other:*
 33: em_htg_mus:*
 34: em_htg_pln:*
 35: em_htg_rod:*
 36: em_htg_mam:*
 37: em_htg_vrt:*
 38: em_sy:*
 39: em_htgo_hum:*
 40: em_htgo_mus:*
 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	% Query		DB	ID	Description
	No.	Score	Match Length		
	1	2773	100.0	1653	6 AX120161 EP 1108790 AX120161 Sequence
	2	2773	100.0	1653	6 BD162278 JP 2002191370 BD162278 Novel pol
	3	2773	100.0	2055	6 AX394566 WO 02/18427 AX394566 Sequence
	4	2773	100.0	340000	1 AP005274 GenBank AP005274 Corynebac
	5	2773	100.0	349980	6 AX120085 EP 1108790 AX120085 Sequence
c	6	1770.5	63.8	87340	1 AP005224 AP005224 Corynebac
c	7	948	34.2	570	6 AX120162 AX120162 Sequence
c	8	948	34.2	570	6 BD162279 BD162279 Novel pol
	9	808	29.1	481	6 AX394568 AX394568 Sequence
	10	685.5	24.7	300550	1 AP005030 AP005030 Streptomy
c	11	684.5	24.7	295150	1 SCO939125 AL939125 Streptomy
c	12	572	20.6	298450	1 SCO939107 AL939107 Streptomy
	13	554	20.0	281450	1 AP005032 AP005032 Streptomy
c	14	520.5	18.8	300100	1 SCO939123 AL939123 Streptomy
	15	518.5	18.7	3962	1 AB024561 AB024561 Bacillus
c	16	518.5	18.7	305153	1 AP001520 AP001520 Bacillus

Nakagawa

Appl. - Mockel

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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 19, 2003, 09:05:58 ; Search time 418 Seconds
(without alignments)
3558.350 Million cell updates/sec

Title: US-09-804-060-2
Perfect score: 2773
Sequence: 1 MSVGGSDWKNFKEVDIIRFA.....IDRGTEDGAVFGVKLPGVME 551

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delect 7.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh

Q=/cgn2_1/USPTO_spool/US09804060/runat_19122003_090551_8495/app_query.fasta_1.71
1

-DB=N_Geneseq_19Jun03 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09804060_@CGN_1_1_0_@runat_19122003_090551_8495 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_19Jun03:*
1: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
4: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
5: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
6: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
7: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
8: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*
9: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*
10: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:*

11: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*
 12: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
 13: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*
 14: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*
 15: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*
 16: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*
 17: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:*
 18: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:*
 19: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*
 20: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
 21: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
 22: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
 23: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
 24: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
 25: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%						
No.	Score	Query	Match	Length	DB	ID		Description	
	1	2773	100.0	1653	22	AAH65042	EP1108790	C glutamicum codin	
	2	2773	100.0	1653	25	ACA01845	DE 10128510	C. glutamicum deri	
	3	2773	100.0	2055	24	AAD35061	W00 02/18427	Corynebacterium gl	
	4	2773	100.0	349980	22	AAH64966	EP 1108790	C glutamicum codin	
c	5	948	34.2	570	22	AAH65043		C glutamicum codin	
	6	808	29.1	481	24	AAD35062		Corynebacterium gl	
	7	462	16.7	1632	22	AAH81447		Escherichia coli p	
	8	449	16.2	1479	24	ABK76973		Bacillus lichenifo	
	9	409.5	14.8	1596	24	ABK76984		Bacillus lichenifo	
	10	409.5	14.8	1596	24	ABK77035		Bacillus lichenifo	
	11	404	14.6	2859	23	AAS93708		DNA encoding novel	
	12	404	14.6	4474	23	AAS88193		DNA encoding novel	
	13	400.5	14.4	1569	24	ABK76985		Bacillus lichenifo	
	14	360.5	13.0	1620	22	AAH47034		Salmonella virulen	
	15	351	12.7	1056	24	AAD27952		Corynebacterium gl	
	16	331.5	12.0	1098	24	ABK76964		Bacillus lichenifo	
	17	323.5	11.7	2061	23	AAS92810		DNA encoding novel	
c	18	322	11.6	1222	23	AAS90320		DNA encoding novel	
	19	320	11.5	2966	20	AAX13283		Enterococcus faeca	
	20	320	11.5	2966	24	ABS99078		Enterococcus faeca	
	21	312.5	11.3	1710	23	AAS74925		DNA encoding novel	
	22	312.5	11.3	1710	23	AAS82063		DNA encoding novel	
	23	312.5	11.3	1710	23	AAS89858		DNA encoding novel	
	24	312.5	11.3	1710	23	AAS90319		DNA encoding novel	
	25	303	10.9	1125	23	AAS82061		DNA encoding novel	
	26	291.5	10.5	959	24	ABK81026		Bacillus clausii g	
	27	291	10.5	1539	24	ABN69517		Streptococcus poly	
	28	278	10.0	1524	24	ABN70545		Streptococcus poly	
	29	278	10.0	1530	24	ABN69516		Streptococcus poly	
	30	278	10.0	2155561	24	ABN71527		Streptococcus poly	
	31	259	9.3	2257	23	AAS89627		DNA encoding novel	
	32	259	9.3	2546	23	AAS90013		DNA encoding novel	

Nakagawa

PK 6/2001

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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 19, 2003, 09:05:59 ; Search time 95 Seconds
(without alignments)
2560.022 Million cell updates/sec

Title: US-09-804-060-2
Perfect score: 2773
Sequence: 1 MSVGGSDWKNFKEVDIIRFA.....IDRGTEDGAVFGVKLPGVME 551

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delect 7.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh

Q=/cg2_1/USPTO_spool/US09804060/runat_19122003_090553_8529/app_query.fasta_1.71
1

-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09804060_@CGN_1_1_56_@runat_19122003_090553_8529 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:*
1: /cg2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cg2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cg2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cg2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cg2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cg2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	%		Query		DB	ID	Description
	No.	Score	Match	Length			
	1	239.5	8.6	912	4	US-09-107-532A-833	Sequence 833, App
	2	213	7.7	876	4	US-09-107-532A-145	Sequence 145, App
	3	204.5	7.4	4403765	3	US-09-103-840A-2	Sequence 2, Appli
	4	204.5	7.4	4411529	3	US-09-103-840A-1	Sequence 1, Appli
	5	198.5	7.2	1854	4	US-09-252-991A-2609	Sequence 2609, Ap
c	6	196.5	7.1	42988	4	US-08-311-731A-128	Sequence 128, App
	7	190.5	6.9	2418	4	US-09-252-991A-2294	Sequence 2294, Ap
	8	190	6.9	1287	4	US-09-252-991A-13923	Sequence 13923, A
	9	190	6.9	4377	3	US-08-911-853-28	Sequence 28, Appl
	10	190	6.9	4377	3	US-09-479-409-28	Sequence 28, Appl
	11	190	6.9	4377	4	US-09-479-453-28	Sequence 28, Appl
c	12	188	6.8	4403765	3	US-09-103-840A-2	Sequence 2, Appli
c	13	188	6.8	4411529	3	US-09-103-840A-1	Sequence 1, Appli
c	14	185.5	6.7	1806	4	US-09-252-991A-2306	Sequence 2306, Ap
	15	181	6.5	1287	4	US-09-252-991A-2964	Sequence 2964, Ap
c	16	181	6.5	1575	4	US-09-252-991A-2723	Sequence 2723, Ap
	17	176	6.3	2283	4	US-09-252-991A-9357	Sequence 9357, Ap
	18	175	6.3	1029	3	US-08-911-853-1	Sequence 1, Appli
	19	175	6.3	1029	3	US-09-479-409-1	Sequence 1, Appli
	20	175	6.3	1029	4	US-09-479-453-1	Sequence 1, Appli
c	21	174	6.3	780	4	US-09-252-991A-13534	Sequence 13534, A
	22	171	6.2	1887	4	US-09-107-532A-3469	Sequence 3469, Ap
	23	170	6.1	2436	4	US-09-252-991A-5645	Sequence 5645, Ap
	24	169	6.1	5175	2	US-08-843-530B-3	Sequence 3, Appli
	25	168.5	6.1	2844	4	US-09-252-991A-12788	Sequence 12788, A
	26	165	6.0	5559	1	US-08-287-442-3	Sequence 3, Appli
	27	165	6.0	5559	1	US-08-459-701-3	Sequence 3, Appli
	28	165	6.0	5559	1	US-08-460-298-3	Sequence 3, Appli
	29	165	6.0	5559	1	US-08-459-174-3	Sequence 3, Appli
	30	165	6.0	5559	5	PCT-US93-06300A-3	Sequence 3, Appli
	31	165	6.0	10763	1	US-08-761-258-1	Sequence 1, Appli
	32	165	6.0	10763	2	US-08-977-306-1	Sequence 1, Appli
	33	163.5	5.9	2295	4	US-09-252-991A-2036	Sequence 2036, Ap
	34	163	5.9	2319	4	US-09-252-991A-15284	Sequence 15284, A
	35	163	5.9	3186	1	US-08-761-258-8	Sequence 8, Appli
	36	163	5.9	3186	2	US-08-977-306-8	Sequence 8, Appli
	37	162.5	5.9	1419	4	US-09-252-991A-5046	Sequence 5046, Ap
c	38	162.5	5.9	1578	4	US-09-252-991A-5039	Sequence 5039, Ap
	39	162.5	5.9	1581	4	US-09-252-991A-5177	Sequence 5177, Ap
	40	161	5.8	2291	1	US-08-920-812-9	Sequence 9, Appli
	41	161	5.8	2291	1	US-08-920-827-9	Sequence 9, Appli
	42	161	5.8	2291	1	US-08-921-177-9	Sequence 9, Appli
	43	161	5.8	2291	1	US-08-362-577C-9	Sequence 9, Appli
	44	161	5.8	2291	2	US-08-920-828-9	Sequence 9, Appli
	45	160.5	5.8	6393	4	US-09-323-872A-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-09-107-532A-833

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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 19, 2003, 10:07:54 ; Search time 1331 Seconds
(without alignments)
1379.447 Million cell updates/sec

Title: US-09-804-060-2
Perfect score: 2773
Sequence: 1 MSVGGSDWKNFKEVDIIRFA.....IDRGTEDGAVFGVKLPGVME 551

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2211978 seqs, 1666101734 residues

Total number of hits satisfying chosen parameters: 4423956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh

Q=/cgn2_1/USPTO_spool/US09804060/runat_19122003_090554_8615/app_query.fasta_1.71
1

-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09804060 @CGN_1_1_353 @runat_19122003_090554_8615
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*

11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
 13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq2:*
 14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
 15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
 16: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
 17: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
 18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

McKagawa
USPAP 2002/01 97605
EE 1108790

Result No.	Score	% Match	Query Length	DB	ID	Description	
	1	2773	100.0	1653	10	US-09-738-626-77	Sequence 77, Appl
	2	2773	100.0	2055	9	US-09-804-060-1	Sequence 1, Appli
	3	2773	100.0	3309400	10	US-09-738-626-1	Sequence 1, Appli
c	4	948	34.2	570	10	US-09-738-626-78	Sequence 78, Appl
	5	808	29.1	481	9	US-09-804-060-3	Sequence 3, Appli
	6	685.5	24.7	1725	15	US-10-156-761-2417	Sequence 2417, Ap
	7	685.5	24.7	9025608	15	US-10-156-761-1	Sequence 1, Appli
	8	552.5	19.9	1695	15	US-10-156-761-2803	Sequence 2803, Ap
	9	462	16.7	1632	9	US-09-741-669-246	Sequence 246, App
	10	449	16.2	1479	10	US-09-974-300-4264	Sequence 4264, Ap
	11	409.5	14.8	1596	10	US-09-974-300-4275	Sequence 4275, Ap
	12	409.5	14.8	1596	10	US-09-974-300-4326	Sequence 4326, Ap
	13	400.5	14.4	1569	10	US-09-974-300-4276	Sequence 4276, Ap
	14	360.5	13.0	1620	13	US-10-182-504-21	Sequence 21, Appl
	15	331.5	12.0	1098	10	US-09-974-300-4255	Sequence 4255, Ap
	16	320	11.5	2966	10	US-09-070-927A-346	Sequence 346, App
	17	319.5	11.5	2772	15	US-10-156-761-774	Sequence 774, App
c	18	319.5	11.5	9025608	15	US-10-156-761-1	Sequence 1, Appli
	19	291.5	10.5	959	10	US-09-974-300-8317	Sequence 8317, Ap
	20	268	9.7	2691	15	US-10-156-761-4135	Sequence 4135, Ap
	21	204.5	7.4	86114	16	US-10-080-170-648	Sequence 648, App
	22	201.5	7.3	1233	10	US-09-712-363-27	Sequence 27, Appl
	23	201	7.2	1563	15	US-10-156-761-3340	Sequence 3340, Ap
	24	199	7.2	1149	10	US-09-974-300-4248	Sequence 4248, Ap
	25	195.5	7.1	1116	10	US-09-738-626-2925	Sequence 2925, Ap
	26	193.5	7.0	1197	10	US-09-738-626-3276	Sequence 3276, Ap
c	27	193.5	7.0	3309400	10	US-09-738-626-1	Sequence 1, Appli
	28	191.5	6.9	1788	9	US-09-815-242-8009	Sequence 8009, Ap
	29	191.5	6.9	1830	9	US-09-815-242-6652	Sequence 6652, Ap
	30	189	6.8	3910	10	US-09-990-337-1	Sequence 1, Appli
	31	189	6.8	3910	13	US-10-411-318-1	Sequence 1, Appli
c	32	188	6.8	45191	16	US-10-080-170-649	Sequence 649, App
	33	184.5	6.7	1497	10	US-09-738-626-842	Sequence 842, App
	34	183.5	6.6	7294	10	US-09-070-927A-63	Sequence 63, Appl
	35	173	6.2	1239	10	US-09-738-626-453	Sequence 453, App
	36	172	6.2	1845	10	US-09-974-300-4239	Sequence 4239, Ap
	37	171.5	6.2	1512	15	US-10-156-761-6752	Sequence 6752, Ap
	38	169	6.1	1359	15	US-10-156-761-130	Sequence 130, App
	39	167	6.0	1161	15	US-10-156-761-6719	Sequence 6719, Ap

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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 19, 2003, 09:05:58 ; Search time 3262 Seconds
(without alignments)
4105.385 Million cell updates/sec

Title: US-09-804-060-2
Perfect score: 2773
Sequence: 1 MSVGGSDWKNFKEVDIIRFA.....IDRGTEDGAVFGVKLPGVME 551

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delect 7.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh

Q=/cgn2_1/USPTO_spool/US09804060/runat_19122003_090552_8515/app_query.fasta_1.71
1

-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09804060_CGN_1_1_2810_runat_19122003_090552_8515 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*

```

11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gssl:*
29: gb_gss2:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%					Query	Description
	No.	Score	Match	Length	ID		
	1	197	7.1	664	9	AV729215	AV729215 AV729215
c	2	190	6.9	500	9	AA399850	AA399850 vd69a12.r
	3	188	6.8	821	9	AV728957	AV728957 AV728957
c	4	179.5	6.5	466	10	BG357782	BG357782 OV2_30_CO
c	5	179.5	6.5	466	10	BG412251	BG412251 OV2_39_F1
c	6	172	6.2	727	10	BE130997	BE130997 L48-1935T
	7	163.5	5.9	689	9	AV728278	AV728278 AV728278
c	8	151	5.4	615	12	BJ063236	BJ063236 BJ063236
	9	150	5.4	329	29	AG019235	AG019235 Homo sapi
	10	148	5.3	423	9	AA645126	AA645126 vs72d10.r
c	11	146	5.3	969	29	CC143810	CC143810 NDL.2707.
c	12	145	5.2	490	29	FR0049133	AL604942 Fugu rubr
	13	140	5.0	870	28	AF029628	AF029628 AF029628
	14	138.5	5.0	796	28	BH401512	BH401512 AG-ND-176
	15	138.5	5.0	1283	29	BZ570078	BZ570078 msh2_1155
	16	138	5.0	449	28	BH396583	BH396583 AG-ND-166
	17	137.5	5.0	1103	29	BZ549247	BZ549247 pacsl-60_
c	18	137	4.9	926	29	BZ552584	BZ552584 pacsl-60_
c	19	135	4.9	971	29	BZ572539	BZ572539 msh2_2680
	20	133.5	4.8	563	28	BH242399	BH242399 ATZFC30TF
	21	131	4.7	499	28	BH370008	BH370008 AG-ND-169
	22	130.5	4.7	1409	29	BZ566619	BZ566619 pacs2-164
c	23	129.5	4.7	675	12	BM411493	BM411493 EST585820
c	24	127	4.6	1477	29	BZ554734	BZ554734 pacsl-60_
	25	126	4.5	1369	11	AY104702	AY104702 Zea mays
c	26	126	4.5	2299	11	AY106831	AY106831 Zea mays
c	27	126	4.5	2598	11	AY103647	AY103647 Zea mays
c	28	123.5	4.5	627	9	AA553607	AA553607 nk78h04.s

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OM nucleic - nucleic search, using sw model

Run on: December 19, 2003, 09:06:22 ; Search time 7379 Seconds
(without alignments)
11393.046 Million cell updates/sec

Title: US-09-804-060-1
Perfect score: 2055
Sequence: 1 tttctgtgtttctcgaaact.....cccgacggcgatggcattga 2055

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2888711 seqs, 20454813386 residues

Word size : 0

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*

DNA Search
using SEQ ID NO:1
OLIGO search

28: em_un:*
 29: em_vi:*
 30: em_htg_hum:*
 31: em_htg_inv:*
 32: em_htg_other:*
 33: em_htg_mus:*
 34: em_htg_pln:*
 35: em_htg_rod:*
 36: em_htg_mam:*
 37: em_htg_vrt:*
 38: em_sy:*
 39: em_htgo_hum:*
 40: em_htgo_mus:*
 41: em_htgo_other:*

Pręđ. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
	1	2055	100.0	2055	6	AX394566	Sequence
	2	2055	100.0	340000	1	AP005274	Corynebac
	3	2055	100.0	349980	6	AX120085	Sequence
	4	1653	80.4	1653	6	AX120161	Sequence
	5	1653	80.4	1653	6	BD162278	Novel pol
c	6	570	27.7	570	6	AX120162	Sequence
c	7	570	27.7	570	6	BD162279	Novel pol
	8	481	23.4	481	6	AX394568	Sequence
	9	400	19.5	1056	6	AX394318	Sequence
	10	200	9.7	654	6	AX120163	Sequence
	11	200	9.7	654	6	BD162280	Novel pol
c	12	92	4.5	601	6	AX066027	Sequence
	13	51	2.5	318	6	AX394320	Sequence
c	14	23	1.1	246543	2	AC097034	Rattus no
c	15	22	1.1	68380	9	AL669854	Human DNA
c	16	22	1.1	76025	2	BX119958	Homo sapi
	17	22	1.1	100000	9	AP000507	Homo sapi
c	18	22	1.1	116320	9	BX248310	Human DNA
c	19	22	1.1	148076	9	AL845443	Human DNA
	20	22	1.1	150295	10	AC127558	Mus muscu
c	21	22	1.1	201568	10	AC122524	Mus muscu
	22	22	1.1	227628	2	AC105812	Rattus no
	23	22	1.1	236822	9	D84394	Homo sapien
c	24	22	1.1	238168	2	AC137275	Rattus no
c	25	22	1.1	256062	2	AC098125	Rattus no
	26	21	1.0	1827	8	AF370494	Arabidops
	27	21	1.0	7133	6	AX251141	Sequence
c	28	21	1.0	8155	9	HUMFGFRZ	Homo sapien
	29	21	1.0	40907	9	AC007459	Homo sapi
	30	21	1.0	41275	9	AC004182	Homo sapi
	31	21	1.0	41277	9	AC004180	Homo sapi
	32	21	1.0	52033	2	AC014228	Drosophil
c	33	21	1.0	87080	8	AC004747	Arabidops

Appl. WO

WO 02/18427
 GenBank
 EP1108790

JP2002191370

EP

JP

WO 02/18427
 WO 02/18596 citB

EP

JP

WO 01/00842

WO 02/18596 citB

Fragment
 Language

3 (Fragment)

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OM nucleic - nucleic search, using sw model

Run on: December 19, 2003, 09:06:22 ; Search time 542 Seconds
(without alignments)
10234.954 Million cell updates/sec

Title: US-09-804-060-1
Perfect score: 2055
Sequence: 1 tttctgtgtttctcgaaact.....cccgacggcgatggcattga 2055

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2552756 seqs, 1349719017 residues

Word size : 0

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : N_Geneseq_19Jun03:*

- 1: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
- 2: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
- 3: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
- 4: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
- 5: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
- 6: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
- 7: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
- 8: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*
- 9: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*
- 10: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:*
- 11: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*
- 12: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
- 13: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*
- 14: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*
- 15: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*
- 16: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*
- 17: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:*
- 18: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:*
- 19: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*
- 20: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
- 21: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
- 22: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
- 23: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
- 24: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
- 25: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Match	Query Length	DB	ID	Description
	1	2055	100.0	2055	24	AAD35061	Corynebacterium gl
	2	2055	100.0	349980	22	AAH64966	C glutamicum codin
	3	1653	80.4	1653	22	AAH65042	C glutamicum codin
	4	1653	80.4	1653	25	ACA01845	C. glutamicum deri
c	5	570	27.7	570	22	AAH65043	C glutamicum codin
	6	481	23.4	481	24	AAD35062	Corynebacterium gl
	7	400	19.5	1056	24	AAD27952	Corynebacterium gl
	8	200	9.7	654	22	AAH65044	C glutamicum codin
	9	200	9.7	654	25	ACA01846	C. glutamicum deri
c	10	92	4.5	601	22	AAF71323	Corynebacterium gl
	11	51	2.5	318	24	AAD27953	Corynebacterium gl
	12	21	1.0	1590	21	AAC39998	Arabidopsis thalia
	13	21	1.0	7133	22	AAS46387	Tumour suppressor
	14	20	1.0	20	24	AAD35063	Corynebacterium gl
c	15	20	1.0	20	24	AAD35064	Corynebacterium gl
	16	20	1.0	20	24	AAD27954	Corynebacterium gl
	17	19	0.9	611	24	ABN60393	Human cancer relat
	18	19	0.9	661	24	ABS64354	Human intestinal p
	19	19	0.9	684	24	ABK69141	DNA encoding human
	20	19	0.9	885	24	ABA99468	Actinoplanes sp DN
	21	19	0.9	1177	24	ABK69140	DNA encoding human
	22	19	0.9	2089	24	ABK69106	DNA encoding human
	23	19	0.9	2248	24	ABS64353	Human intestinal p
c	24	19	0.9	38064	24	ABA99469	Actinoplanes sp SE
c	25	18	0.9	181	21	AAC17167	Human secreted pro
	26	18	0.9	256	21	AAC06619	Human secreted pro
c	27	18	0.9	269	25	ABX29197	Human GDP-mannose
c	28	18	0.9	391	21	AAC30873	Human secreted pro
c	29	18	0.9	434	22	AAI88630	Human polynucleoti
c	30	18	0.9	482	25	ABZ56253	Aspergillus oryzae
c	31	18	0.9	493	24	ABL69526	Prostate cancer re
	32	18	0.9	628	22	AAS64095	Human prostate cDN
	33	18	0.9	628	24	ABL95466	Human prostate-spe
	34	18	0.9	628	25	ACA59903	Prostate cancer th
c	35	18	0.9	664	21	AAF14457	Aspergillus oryzae
c	36	18	0.9	817	24	ABL01349	Murine apoptosis r
	37	18	0.9	872	22	AAH32214	Human olfactory re
c	38	18	0.9	975	22	AAH67537	C glutamicum codin
c	39	18	0.9	993	25	ACA01189	C. glutamicum deri
c	40	18	0.9	1001	21	AAC57511	Arachidonic acid m
c	41	18	0.9	1002	21	AAC57946	Arachidonic acid m
	42	18	0.9	1104	20	AAX19102	Rhodospiridium tor
	43	18	0.9	1107	17	AAT38221	D-amino acid oxida
c	44	18	0.9	1125	23	ABL03095	Drosophila melanog
	45	18	0.9	1161	21	AAC45666	Arabidopsis thalia
	46	18	0.9	1163	21	AAC33253	Arabidopsis thalia
	47	18	0.9	1335	25	ABZ38497	N. gonorrhoeae nuc
c	48	18	0.9	1348	25	ACA57089	Human adipocyte Se
c	49	18	0.9	1443	21	AAC46127	Arabidopsis thalia

Appl.

PR 6/2001

WO 02/18427

EP 1108770

"

DE 10128510

EP

WO 02/18427

WO 02/18596 - PR 2/2001

EP

DE 10128510

WO 01/00842

WO 02/18596

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OM nucleic - nucleic search, using sw model

Run on: December 19, 2003, 09:06:22 ; Search time 3931 Seconds
(without alignments)
12705.596 Million cell updates/sec

Title: US-09-804-060-1
Perfect score: 2055
Sequence: 1 tttctgtgtttctcgaaact.....cccgacggcgatggcattga 2055

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 22781392 seqs, 12152238056 residues

Word size : 0

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : EST:*

- 1: em_estba:*
- 2: em_esthum:*
- 3: em_estin:*
- 4: em_estmu:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_htc:*
- 9: gb_est1:*
- 10: gb_est2:*
- 11: gb_htc:*
- 12: gb_est3:*
- 13: gb_est4:*
- 14: gb_est5:*
- 15: em_estfun:*
- 16: em_estom:*
- 17: em_gss_hum:*
- 18: em_gss_inv:*
- 19: em_gss_pln:*
- 20: em_gss_vrt:*
- 21: em_gss_fun:*
- 22: em_gss_mam:*
- 23: em_gss_mus:*
- 24: em_gss_pro:*
- 25: em_gss_rod:*
- 26: em_gss_phg:*
- 27: em_gss_vrl:*

28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	%		DB	ID	Description
			Query	Match Length			
c	1	24	1.2	900	28	BH166924	BH166924 ENTRV64TF
c	2	24	1.2	902	28	BH166784	BH166784 ENTRY71TF
	3	21	1.0	489	29	BZ353303	BZ353303 SALK_1201
	4	21	1.0	514	10	BF573785	BF573785 602075764
	5	21	1.0	556	9	AW168094	AW168094 xg59h04.x
	6	21	1.0	836	10	BF212072	BF212072 601812886
c	7	21	1.0	1652	12	BG764440	BG764440 602736463
c	8	20	1.0	190	10	BB577346	BB577346 BB577346
	9	20	1.0	248	10	BE637249	BE637249 WHE1295-1
	10	20	1.0	250	10	BG157184	BG157184 sab23f02.
	11	20	1.0	276	10	BE494139	BE494139 WHE1251_F
c	12	20	1.0	294	10	BG268668	BG268668 1000207E0
	13	20	1.0	350	9	AU251628	AU251628 AU251628
	14	20	1.0	358	10	BF145420	BF145420 WHE1841-1
	15	20	1.0	361	10	BE496020	BE496020 WHE1260_C
	16	20	1.0	379	10	BE494545	BE494545 WHE1256_A
	17	20	1.0	409	10	BG264074	BG264074 WHE1812_E
	18	20	1.0	411	10	BF429450	BF429450 WHE1803_C
	19	20	1.0	417	10	BF146185	BF146185 WHE1839_B
c	20	20	1.0	418	14	M89319	M89319 CEL21A4 Chr
	21	20	1.0	444	10	BE493833	BE493833 WHE1275_A
	22	20	1.0	454	10	BE637234	BE637234 WHE1806_A
	23	20	1.0	459	10	BF145287	BF145287 WHE1834_g
	24	20	1.0	468	10	BE494339	BE494339 WHE1253_C
	25	20	1.0	469	10	BF145464	BF145464 WHE1835_F
	26	20	1.0	484	13	BQ452970	BQ452970 sao94a07.
	27	20	1.0	498	10	BE495065	BE495065 WHE1267_C
	28	20	1.0	501	10	BE494115	BE494115 WHE1251_H
	29	20	1.0	514	10	BE495320	BE495320 WHE1268_D
	30	20	1.0	518	10	BE494582	BE494582 WHE1255_F
c	31	20	1.0	527	28	AQ435051	AQ435051 HS_5114_B
	32	20	1.0	531	10	BE493922	BE493922 WHE1276_A
	33	20	1.0	542	10	BE494855	BE494855 WHE1258_E
c	34	20	1.0	545	10	BF145561	BF145561 WHE1841-1
c	35	20	1.0	548	28	AQ435046	AQ435046 HS_5114_B
c	36	20	1.0	569	28	AQ641399	AQ641399 RPCI93-Dp
	37	20	1.0	570	10	BE495147	BE495147 WHE1274_C
	38	20	1.0	577	10	BF145666	BF145666 WHE1838_C
	39	20	1.0	589	10	BE060082	BE060082 HVSMEg001
	40	20	1.0	592	10	BF145803	BF145803 WHE1840_H
c	41	20	1.0	619	14	CD227504	CD227504 CCC1_51_B
	42	20	1.0	620	29	BZ624822	BZ624822 ig93g04.g
	43	20	1.0	634	10	BE493840	BE493840 WHE1275_A
c	44	20	1.0	641	29	BZ624821	BZ624821 ig93g04.b
	45	20	1.0	644	10	BE493931	BE493931 WHE1276_A

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OM nucleic - nucleic search, using sw model

Run on: December 19, 2003, 09:06:22 ; Search time 146 Seconds
 (without alignments)
 6212.619 Million cell updates/sec

Title: US-09-804-060-1
 Perfect score: 2055
 Sequence: 1 tttctgtgtttctcgaaact.....cccgacggcgatggcattga 2055

Scoring table: OLIGO_NUC
 Gapop 60.0 , Gapext 60.0

Searched: 569978 seqs, 220691566 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : Issued_Patents_NA:*
 1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
 2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
 3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
 4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
 5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
 6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%							
Result		Query							
No.	Score	Match	Length	DB	ID	Description			
c	1	19	0.9	537	4	US-09-328-352-170	Sequence 170, App		
	2	19	0.9	2373	4	US-09-328-352-157	Sequence 157, App		
c	3	18	0.9	1001	4	US-09-641-638-145	Sequence 145, App		
c	4	18	0.9	1002	4	US-09-641-638-580	Sequence 580, App		
	5	18	0.9	1104	2	US-08-903-624-2	Sequence 2, Appli		
	6	18	0.9	1104	3	US-08-973-914-8	Sequence 8, Appli		
	7	18	0.9	1107	2	US-08-732-461-1	Sequence 1, Appli		
	8	18	0.9	1458	2	US-08-903-624-1	Sequence 1, Appli		
c	9	18	0.9	4403765	3	US-09-103-840A-2	Sequence 2, Appli		
c	10	18	0.9	4411529	3	US-09-103-840A-1	Sequence 1, Appli		
c	11	17	0.8	513	4	US-09-387-286-23	Sequence 23, Appl		

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OM nucleic - nucleic search, using sw model

Run on: December 19, 2003, 11:19:12 ; Search time 2431 Seconds
(without alignments)
2816.815 Million cell updates/sec

Title: US-09-804-060-1
Perfect score: 2055
Sequence: 1 tttctgtgtttctcgaaact.....cccgacggcgatggcattga 2055

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2211978 seqs, 1666101734 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4423956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : Published_Applications_NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq2:*
- 14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

2002/0197605

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2055	100.0	2055	9	US-09-804-060-1	Sequence 1, Appli
2	2055	100.0	3309400	10	US-09-738-626-1	Sequence 1, Appli
3	1653	80.4	1653	10	US-09-738-626-77-	Sequence 77, Appl
c 4	570	27.7	570	10	US-09-738-626-78-	Sequence 78, Appl
5	481	23.4	481	9	US-09-804-060-3	Sequence 3, Appli
6	200	9.7	654	10	US-09-738-626-79-	Sequence 79, Appl
7	20	1.0	20	9	US-09-804-060-4	Sequence 4, Appli
c 8	20	1.0	20	9	US-09-804-060-5	Sequence 5, Appli
c 9	19	0.9	571	13	US-10-027-632-95825	Sequence 95825, A
c 10	19	0.9	571	14	US-10-027-632-95825	Sequence 95825, A
11	19	0.9	661	10	US-09-729-454-11	Sequence 11, Appl
12	19	0.9	1961	13	US-10-027-632-175244	Sequence 175244,
13	19	0.9	1961	14	US-10-027-632-175244	Sequence 175244,
14	19	0.9	2248	10	US-09-729-454-10	Sequence 10, Appl
c 15	18	0.9	269	10	US-09-878-574-11256	Sequence 11256, A
16	18	0.9	446	11	US-09-918-995-22915	Sequence 22915, A
c 17	18	0.9	461	11	US-09-918-995-32836	Sequence 32836, A
c 18	18	0.9	469	11	US-09-918-995-33991	Sequence 33991, A
c 19	18	0.9	493	10	US-09-969-708-392	Sequence 392, App
c 20	18	0.9	604	13	US-10-027-632-134834	Sequence 134834,
c 21	18	0.9	604	14	US-10-027-632-134834	Sequence 134834,
c 22	18	0.9	620	13	US-10-027-632-43496	Sequence 43496, A
c 23	18	0.9	620	14	US-10-027-632-43496	Sequence 43496, A
24	18	0.9	628	9	US-09-759-143-762	Sequence 762, App
25	18	0.9	628	9	US-09-780-669-762	Sequence 762, App
26	18	0.9	628	9	US-09-822-827-762	Sequence 762, App
27	18	0.9	628	10	US-09-895-793-762	Sequence 762, App
28	18	0.9	628	10	US-09-895-814-762	Sequence 762, App
29	18	0.9	628	13	US-10-144-678A-762	Sequence 762, App
30	18	0.9	628	13	US-10-294-025-762	Sequence 762, App
31	18	0.9	628	14	US-10-012-896-762	Sequence 762, App
32	18	0.9	637	13	US-10-027-632-191408	Sequence 191408,
33	18	0.9	637	13	US-10-027-632-191409	Sequence 191409,
34	18	0.9	637	14	US-10-027-632-191408	Sequence 191408,
35	18	0.9	637	14	US-10-027-632-191409	Sequence 191409,
c 36	18	0.9	840	13	US-10-027-632-157360	Sequence 157360,
c 37	18	0.9	840	14	US-10-027-632-157360	Sequence 157360,
c 38	18	0.9	975	10	US-09-738-626-2572	Sequence 2572, Ap
c 39	18	0.9	1001	12	US-10-170-097-145	Sequence 145, App
c 40	18	0.9	1002	12	US-10-170-097-580	Sequence 580, App
c 41	18	0.9	1362	15	US-10-156-761-575	Sequence 575, App
c 42	18	0.9	1584	9	US-09-925-297-125	Sequence 125, App
43	18	0.9	1947	15	US-10-156-761-7287	Sequence 7287, Ap
c 44	18	0.9	2001	13	US-10-190-312A-77	Sequence 77, Appl
c 45	18	0.9	2517	13	US-10-027-632-111576	Sequence 111576,
c 46	18	0.9	2517	14	US-10-027-632-111576	Sequence 111576,
c 47	18	0.9	2939	14	US-10-044-090-350	Sequence 350, App
48	18	0.9	4372	10	US-09-993-811-1	Sequence 1, Appli
49	18	0.9	4372	16	US-10-254-010-3	Sequence 3, Appli
50	18	0.9	6823	10	US-09-989-920-16	Sequence 16, Appl
51	18	0.9	20247	10	US-09-764-877-2680	Sequence 2680, Ap